

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/245,198

1633

DATE: 05/19/2000
 TIME: 18:42:50

INPUT SET: S35512.raw

#10

**This Raw Listing contains the General
 Information Section and up to the first 5 pages.**

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Chicheportiche, Yves
 Browning, Jeffrey L.

(ii) TITLE OF INVENTION: A TUMOR NECROSIS FACTOR RELATED LIGAND

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BIOGEN, INC.
- (B) STREET: 14 CAMBRIDGE CENTER
- (C) CITY: CAMBRIDGE
- (D) STATE: MA
- (E) COUNTRY: US
- (F) ZIP: 02142

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: not yet assigned
- (B) FILING DATE: 07-May-1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: FLYNN, KERRY A.
- (B) REGISTRATION NUMBER: 33,693
- (C) REFERENCE/DOCKET NUMBER: A003 PCT CIP TECH CENTER 1600/2900

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 679-3583
- (B) TELEFAX: (617) 679-2838

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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47         (D) TOPOLOGY: linear
48
49         (ii) MOLECULE TYPE: cDNA
50
51         (iii) HYPOTHETICAL: NO
52
53         (iv) ANTI-SENSE: NO
54
55         (vi) ORIGINAL SOURCE:
56             (A) ORGANISM: TNF family related protein
57
58         (ix) FEATURE:
59             (A) NAME/KEY: CDS
60             (B) LOCATION: 2..676
61
62
63         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65     G GTG CTG AGC CTG GGC CTG GCG CTG GCC TGC CTT GGC CTC CTG CTG      46
66     Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu
67     1             5             10             15
68
69     GTC GTG GTC AGC CTG GGG AGC TGG GCA ACG CTG TCT GCC CAG GAG CCT      94
70     Val Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro
71             20             25             30
72
73     TCT CAG GAG GAG CTG ACA GCA GAG GAC CGC CGG GAG CCC CCT GAA CTG      142
74     Ser Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu
75             35             40             45
76
77     AAT CCC CAG ACA GAG GAA AGC CAG GAT GTG GTA CCT TTC TTG GAA CAA      190
78     Asn Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln
79             50             55             60
80
81     CTA GTC CGG CCT CGA AGA AGT GCT CCT AAA GGC CGG AAG GCG CGG CCT      238
82     Leu Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro
83             65             70             75
84
85     CGC CGA GCT ATT GCA GCC CAT TAT GAG GTT CAT CCT CGG CCA GGA CAG      286
86     Arg Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln
87     80             85             90             95
88
89     GAT GGA GCA CAA GCA GGT GTG GAT GGG ACA GTG AGT GGC TGG GAA GAG      334
90     Asp Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu
91             100             105             110
92
93     ACC AAA ATC AAC AGC TCC AGC CCT CTG CGC TAC GAC CGC CAG ATT GGG      382
94     Thr Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly
95             115             120             125
96
97     GAA TTT ACA GTC ATC AGG GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG      430
98     Glu Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val
99             130             135             140

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100
101 CAC TTT GAT GAG GGA AAG GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG 478
102 His Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val
103 145 150 155
104
105 AAC GGT GTG CTG GCC CTG CGC TGC CTG GAA GAA TTC TCA GCC ACA GCA 526
106 Asn Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala
107 160 165 170 175
108
109 GCA AGC TCT CCT GGG CCC CAG CTC CGT TTG TGC CAG GTG TCT GGG CTG 574
110 Ala Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu
111 180 185 190
112
113 TTG CCG CTG CGG CCA GGG TCT TCC CTT CGG ATC CGC ACC CTC CCC TGG 622
114 Leu Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp
115 195 200 205
116
117 GCT CAT CTT AAG GCT GCC CCC TTC CTA ACC TAC TTT GGA CTC TTT CAA 670
118 Ala His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln
119 210 215 220
120
121 GTT CAC TGAGGGGCCT TGCTCTCCCA GATTCCTTAA ACTTTCCCTG GCTCCAGGAG 726
122 Val His
123 225
124
125 CATCACCACA CCTCCCTACC CCACCCCCAC TCCTCCACCC CCTCGCTGCT CCTTGGTCCA 786
126
127 GTCCTGTCTC TCCTCAAAGG CAGCCAGAGC TTGTTCACAT GTTTCCATTC CACAGACGTA 846
128
129 TCCTTGCTCT TCTTAACATC CCATCCCACC ACAACTATCC ACCTCACTAG CTCCCAAAGC 906
130
131 CCCTACTTAT CCCTGACTCC CCCACCCACT CACCCGACCA CGTGTTTATT GACTTTGTGC 966
132
133 ACCAGGCACT GAGATGGGCT GGACCTGGTG GCAGGAAGCC AGAGAACCTG GGACTAGGCC 1026
134
135 AGAAGTTCCC AACTGTGAGG GGAAGAGCT GGGGACAAGC TCCTCCCTGG ATCCCTGTGG 1086
136
137 ATTTTGAAAA GATACTATTT TTATTATTAT TGTGACAAAA TGTAAATGG ATATTAAAGA 1146
138
139 GAATAAATCA TGATTTCTCT TC 1168
140
141
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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153 Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Val
154 1 5 10 15
155
156 Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro Ser
157 20 25 30
158
159 Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu Asn
160 35 40 45
161
162 Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln Leu
163 50 55 60
164
165 Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro Arg
166 65 70 75 80
167
168 Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
169 85 90 95
170
171 Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Thr
172 100 105 110
173
174 Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly Glu
175 115 120 125
176
177 Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
178 130 135 140
179
180 Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asn
181 145 150 155 160
182
183 Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
184 165 170 175
185
186 Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
187 180 185 190
188
189 Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
190 195 200 205
191
192 His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
193 210 215 220
194
195 His
196 225
197

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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206      (ii) MOLECULE TYPE: cDNA
207
208      (iii) HYPOTHETICAL: NO
209
210      (iv) ANTI-SENSE: NO
211
212      (vi) ORIGINAL SOURCE:
213          (A) ORGANISM: TNF family related protein
214
215      (ix) FEATURE:
216          (A) NAME/KEY: CDS
217          (B) LOCATION: 1..852
218
219
220      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
221
222      ATG TCA TTG TTA GAC TTT GAA ATT TCC GCC CGC CGG CTC CCC CTC CCC      48
223      Met Ser Leu Leu Asp Phe Glu Ile Ser Ala Arg Arg Leu Pro Leu Pro
224          1              5              10              15
225
226      CGA TCC CTC GGG TCC CGG GAT GGG GGG GCG GTG AGG CAG GCA CAG CCC      96
227      Arg Ser Leu Gly Ser Arg Asp Gly Gly Ala Val Arg Gln Ala Gln Pro
228          20              25              30
229
230      CCC GCC CCC ATG GCC GCC CGT CGG AGC CAG AGG CGG AGG GGG CGC CGG      144
231      Pro Ala Pro Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg
232          35              40              45
233
234      GGG GAG CCG GGC ACC GCC CTG CTG GTC CCG CTC GCG CTG GGC CTG GGC      192
235      Gly Glu Pro Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly
236          50              55              60
237
238      CTG GCG CTG GCC TGC CTC GGC CTC CTG CTG GCC GTG GTC AGT TTG GGG      240
239      Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly
240          65              70              75              80
241
242      AGC CGG GCA TCG CTG TCC GCC CAG GAG CCT GCC CAG GAG GAG CTG GTG      288
243      Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val
244          85              90              95
245
246      GCA GAG GAG GAC CAG GAC CCG TCG GAA CTG AAT CCC CAG ACA GAA GAA      336
247      Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu
248          100              105              110
249
250      AGC CAG GAT CCT GCG CCT TTC CTG AAC CGA CTA GTT CGG CCT CGC AGA      384
251      Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg
252          115              120              125
253
254      AGT GCA CCT AAA GGC CGG AAA ACA CGG GCT CGA AGA GCG ATC GCA GCC      432
255      Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala
256          130              135              140
257
258      CAT TAT GAA GTT CAT CCA CGA CCT GGA CAG GAC GGA GCG CAG GCA GGT      480

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: not yet assigned